

SEQUENCE LISTING

<110> Hemmati-Brivanlou, Ali
Weinstein, Daniel C.

<120> TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE
THEREOF

<130> 600-1-211 N

<140> UNASSIGNED
<141> 1999-05-25

<160> 12

<170> PatentIn Ver. 2.0

<210> 1
<211> 1245
<212> DNA
<213> Xenopus laevis

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cagtgtttgg atattcagat ccgtgaaacc caaggcttga ttttagcacc caccaaagag 360
ttagcacggc aaattcagaa ggtgttgctt gctttgggg actacatgaa tgtgcagtgt 420
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cacgttgcgtt ctggAACacc agggcgtgtt tttgatatga ttcgacgcag aagtttaaga 540
actcgggcca ttaaaatgtt agtgctggat gaagctgatg aaatgttcaa taagggttcc 600
aaggagcaaa ttatgatgt atacaggtat ctgcctccag caacacaagt ttgtttaatc 660
agtgcatacc tgccacatga aatcctggaa atgaccaata agtttatgac tgatcccattc 720
cgtatccttg tgaaacgtgta tgagttgaca ctggaaaggca tcaaggcgtt ttttgcgtt 780
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agagaagcaa atttcacagt ttgcgtcaatg catgggtgata tgcccaaaaa ggagagagag 960
tcaatcatga aagaattccg atctggtgca agccgagtcc tcataatcaac ggacgtctgg 1020
gccccgaggat tggatgtgcc acaggcttcc ttgattatca actatgatct tcccaataac 1080
cgagaattgt acattcacag aattggccga tcaggaagat atggaagaaa ggggttgcc 1140
attaactttg tcaagaatga tgacatccgt attttaagag atattgagca gtactattcg 1200
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<210> 2
<211> 415
<212> PRT

<213> Xenopus laevis

<400> 2

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| Met | Ala | Ala | Ala | Ala | Val | Ala | Gly | Val | Ala | Gly | Leu | Thr | Thr | Ala | His |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |
| Ala | Lys | Arg | Leu | Leu | Arg | Glu | Glu | Asp | Met | Thr | Thr | Val | Glu | Phe | Gln |
| | 20 | | | | | 25 | | | | | | 30 | | | |
| Thr | Ser | Glu | Glu | Val | Asp | Val | Thr | Pro | Thr | Phe | Asp | Thr | Met | Gly | Leu |
| | 35 | | | | | 40 | | | | | | 45 | | | |
| Arg | Glu | Asp | Leu | Leu | Arg | Gly | Ile | Tyr | Ala | Tyr | Gly | Phe | Glu | Lys | Pro |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ser | Ala | Ile | Gln | Gln | Lys | Ala | Ile | Lys | Gln | Ile | Ile | Lys | Gly | Arg | Asp |
| | 65 | | | | | 70 | | | | 75 | | | 80 | | |
| Val | Ile | Ala | Gln | Ser | Gln | Ser | Gly | Thr | Gly | Lys | Thr | Ala | Thr | Phe | Cys |
| | | | | 85 | | | | 90 | | | | 95 | | | |
| Val | Ser | Val | Leu | Gln | Cys | Leu | Asp | Ile | Gln | Ile | Arg | Glu | Thr | Gln | Ala |
| | | | | 100 | | | | 105 | | | | 110 | | | |
| Leu | Ile | Leu | Ala | Pro | Thr | Lys | Glu | Leu | Ala | Arg | Gln | Ile | Gln | Lys | Val |
| | | | | 115 | | | | 120 | | | | 125 | | | |
| Leu | Leu | Ala | Leu | Gly | Asp | Tyr | Met | Asn | Val | Gln | Cys | His | Ala | Cys | Ile |
| | | | | 130 | | | | 135 | | | 140 | | | | |
| Gly | Gly | Thr | Asn | Val | Gly | Glu | Asp | Ile | Arg | Lys | Leu | Asp | Tyr | Gly | Gln |
| | 145 | | | | 150 | | | | 155 | | | 160 | | | |
| His | Val | Val | Ala | Gly | Thr | Pro | Gly | Arg | Val | Phe | Asp | Met | Ile | Arg | Arg |
| | | | | 165 | | | | 170 | | | 175 | | | | |
| Arg | Ser | Leu | Arg | Thr | Arg | Ala | Ile | Lys | Met | Leu | Val | Leu | Asp | Glu | Ala |
| | | | | 180 | | | | 185 | | | 190 | | | | |
| Asp | Glu | Met | Leu | Asn | Lys | Gly | Phe | Lys | Glu | Gln | Ile | Tyr | Asp | Val | Tyr |
| | | | | 195 | | | | 200 | | | 205 | | | | |
| Arg | Tyr | Leu | Pro | Pro | Ala | Thr | Gln | Val | Cys | Leu | Ile | Ser | Ala | Thr | Leu |
| | | | | 210 | | | | 215 | | | 220 | | | | |
| Pro | His | Glu | Ile | Leu | Glu | Met | Thr | Asn | Lys | Phe | Met | Thr | Asp | Pro | Ile |
| | 225 | | | | 230 | | | | 235 | | | 240 | | | |

| | | |
|-----------------------------------------------------------------|-----|-----|
| Arg Ile Leu Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln | | |
| 245 | 250 | 255 |
| | | |
| Phe Phe Val Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys | | |
| 260 | 265 | 270 |
| | | |
| Asp Leu Tyr Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn | | |
| 275 | 280 | 285 |
| | | |
| Thr Lys Arg Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn | | |
| 290 | 295 | 300 |
| | | |
| Phe Thr Val Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu | | |
| 305 | 310 | 315 |
| 320 | | |
| | | |
| Ser Ile Met Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser | | |
| 325 | 330 | 335 |
| | | |
| Thr Asp Val Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile | | |
| 340 | 345 | 350 |
| | | |
| Ile Asn Tyr Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile | | |
| 355 | 360 | 365 |
| | | |
| Gly Arg Ser Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val | | |
| 370 | 375 | 380 |
| | | |
| Lys Asn Asp Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser | | |
| 385 | 390 | 395 |
| 400 | | |
| | | |
| Thr Gln Ile Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile Glx | | |
| 405 | 410 | 415 |

<210> 3
 <211> 532
 <212> DNA
 <213> Homo sapiens

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 ttgatcttgg ctcccacaag agagttggct gtgcagatcc agaaggggct gcttgctctc 180
 ggtgactaca tgaatgtcca gtgccatgcc tgcattggag gcaccaatgt tggcgaggac 240
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 atgattcgtc gcagaaggct aaggacacgt gctatcaaaa tggatggttt ggatgaagct 360
 gatgaaatgt tgaataaagg tttcaaagag cagattacg atgtatacag gtacctgcct 420
 ccagccacac aggtggttct catcagtgcc acgctgccac acgagattct ggagatgacc 480

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<212> PRT
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Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu Ala Pro Thr Arg Glu
35 40 45

Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala Leu Gly Asp Tyr Met
50 55 60

Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr Asn Val Gly Glu Asp
65 70 75 80

Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val Ala Gly Thr Pro Gly
85 90 95

Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu Arg Thr Arg Ala Ile
100 105 110

Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Lys Gly Phe
115 120 125

Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu Pro Pro Ala Thr Gln
130 135 140

Val Val Leu Ile Ser Ala Thr Leu Pro His Glu Ile Leu Glu Met Thr
145 150 155 160

Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu Val Gly Ile Pro Ala
165 170 175

Ala

<210> 5
<211> 1536
<212> DNA

<213> Homo sapiens

<400> 5

<210> 6

<211> 411

<212> PRT

<213> *Homo sapiens*

<400> 6

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5

10

15

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 20 25 30

20

25

3

Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp
35 40 45

35

40

10

Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile
50 55 60

50

55

- 60 -

Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala
65 70 75 80

Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val
85 90 95

Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu
100 105 110

Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala
115 120 125

Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr
130 135 140

Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val
145 150 155 160

Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu
165 170 175

Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met
180 185 190

Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu
195 200 205

Pro Ser Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu
210 215 220

Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu
225 230 235 240

Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val
245 250 255

Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr
260 265 270

Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg
275 280 285

Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val
290 295 300

Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met
305 310 315 320

Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val

325

330

335

Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr

340

345

350

Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser

355

360

365

Gly Gln Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp

370

375

380

Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile

385

390

395

400

Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile

405

410

<210> 7

<211> 1682

<212> DNA

<213> Homo sapiens

<400> 7

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ggcgccgcgt gtgctttcc gcccactctg aatcatggcg accacggcca cgatggcgcac 240
ctcggtctcg gcgcgaaagc ggctgctcaa agaggaagac atgactaaag tggattcga 300
gaccagcggag gaggtggatg tgaccccccac gttcgacacc atgggcctgc gggaggac 360
gctgcggggc atctacgctt acggtttga aaaaccatca gcaatccagc aacgagcaat 420
caagcagatc atcaaaggga gagatgtcat cgcacagtct cagtccggca caggaaaaac 480
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cggtgactac atgaatgtcc agtgccatgc ctgcatttgc ggcaccaatg ttggcgagga 660
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tatgattcgt cgcagaagcc taaggacacg tgctatcaa atgttggtt tggatgaagc 780
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tcgatacggc cggaaagggtg tggccattaa ctttgtaaag aatgacgaca tccgcattc 1380

cagagatatac gagcagtaact atccactca gattgatgag atgcccgtga acgttgctga 1440
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gttggaaatg attagatcc agattctact taatgggtt tatatggact ttcttctcat 1560
aaatggcctg ccgtctccct tccttgaag aggatatggg gattctgctc tctttctta 1620
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at 1682

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<211> 411
<212> PRT
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Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp
35 40 45

Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile
50 55 60

Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala
65 70 75 80

Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val
85 90 95

Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu
100 105 110

Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala
115 120 125

Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr
130 135 140

Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val
145 150 155 160

Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu
165 170 175

Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met
180 185 190

Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu
195 200 205

Pro Pro Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu
210 215 220

Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu
225 230 235 240

Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val
245 250 255

Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr
260 265 270

Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg
275 280 285

Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val
290 295 300

Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met
305 310 315 320

Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val
325 330 335

Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr
340 345 350

Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser
355 360 365

Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp
370 375 380

Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile
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Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile
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<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 10
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<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 11
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<210> 12
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<220>
<223> Description of Artificial Sequence:primer

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